

Fig.1

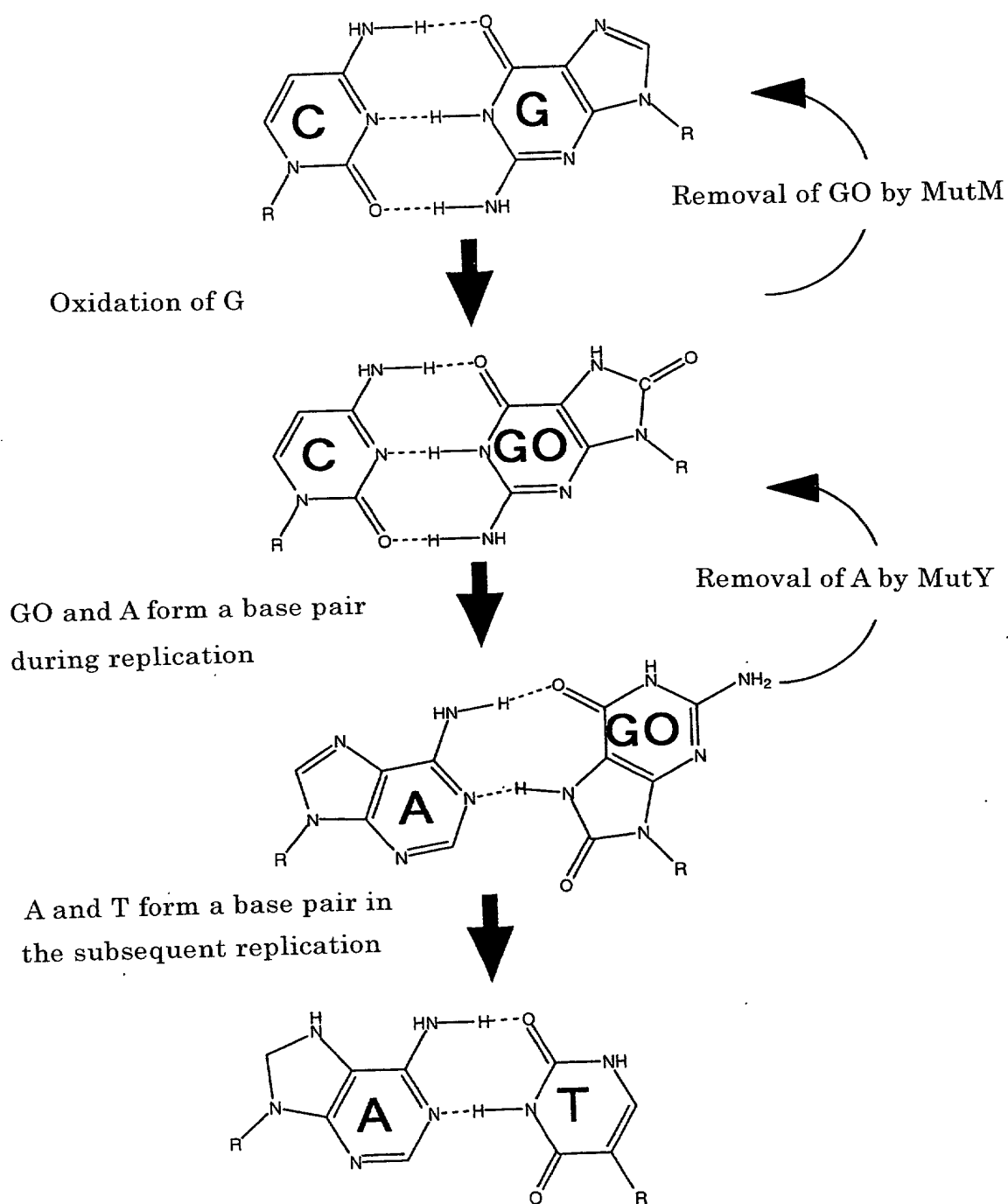


Fig.2

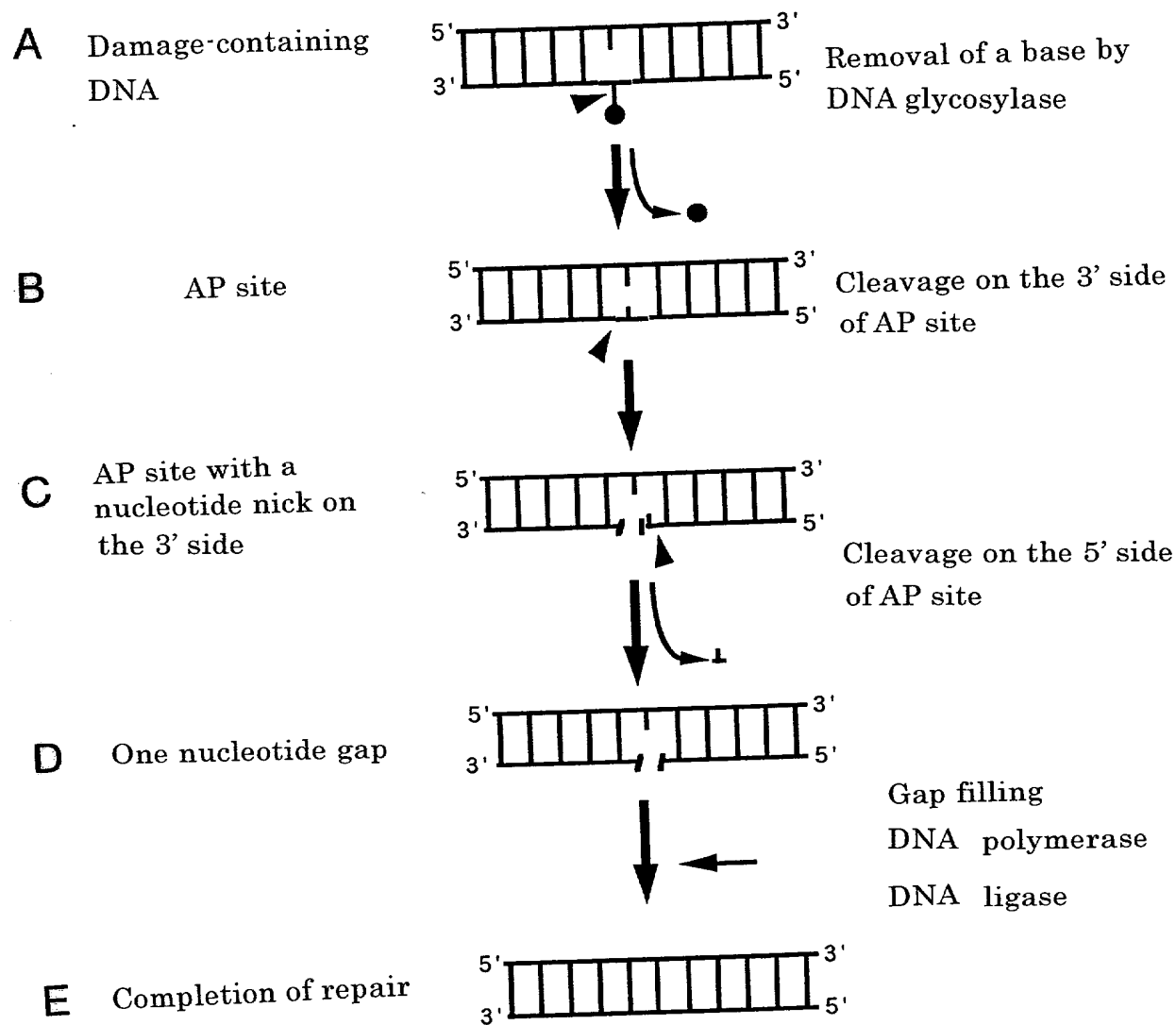


Fig.3

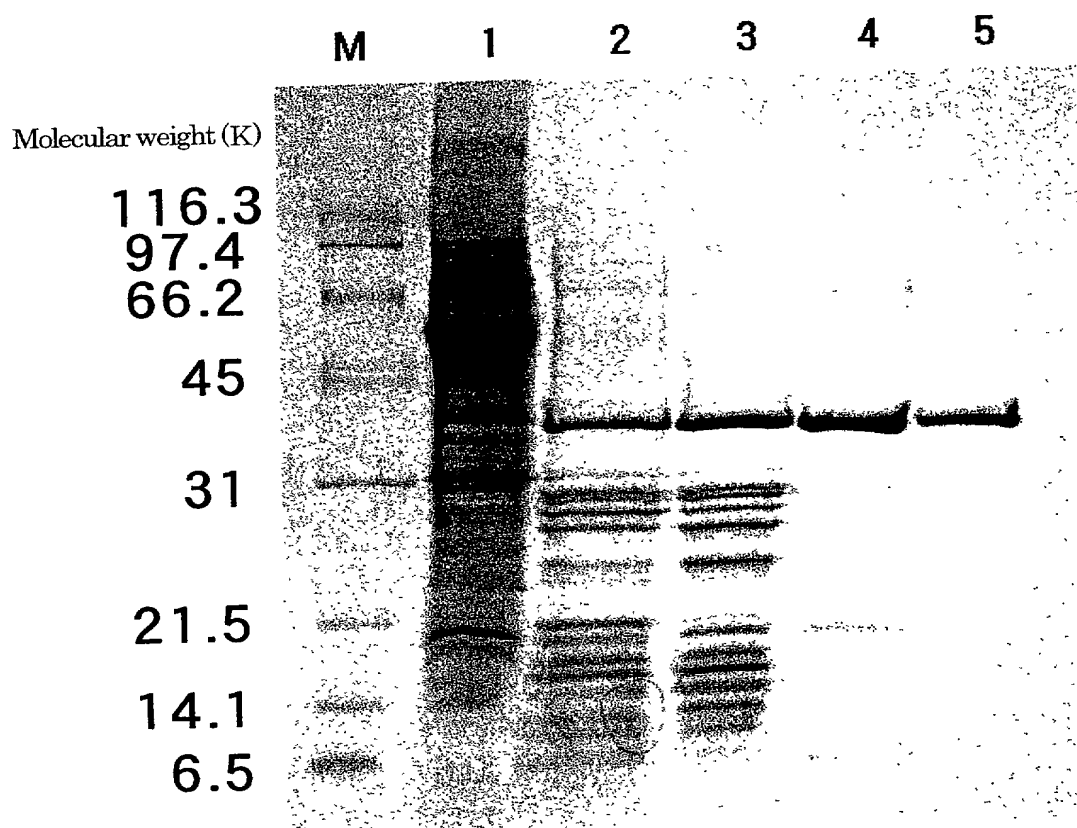


Fig.4

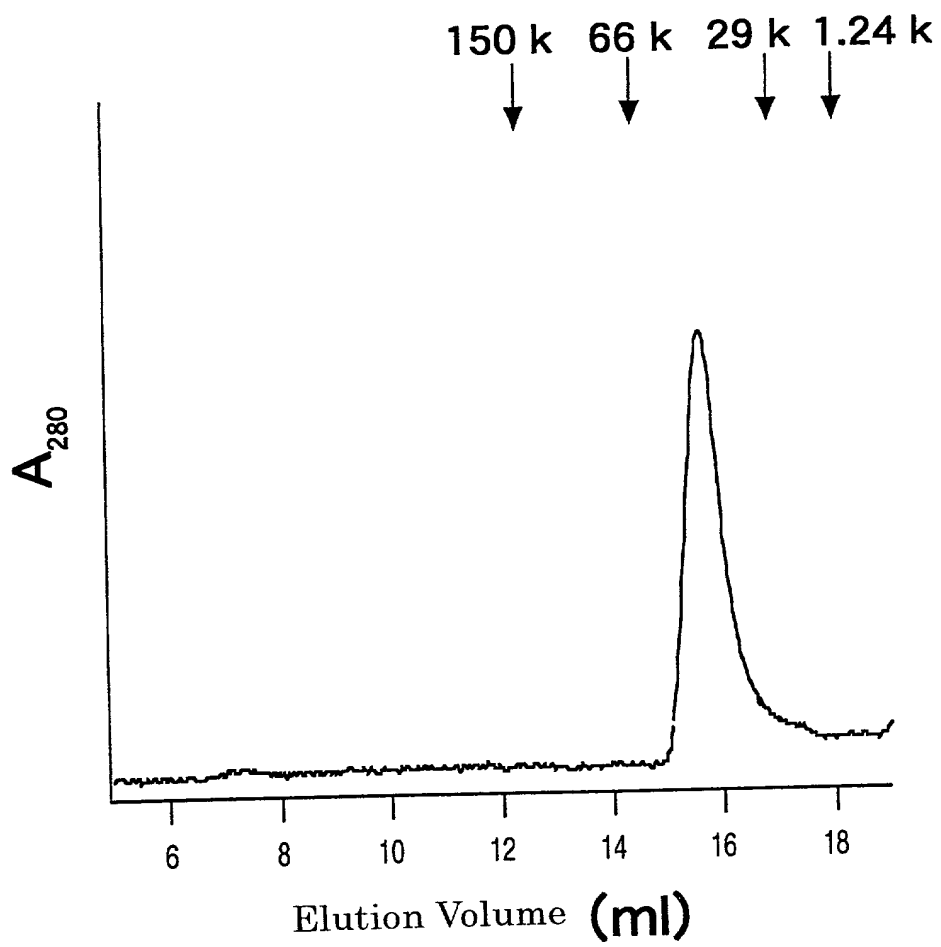


Fig.5

Tth MutY	1	MEAWRKALIAVIR	CE	KDPYRVLYSEVLQOTRVEOALPYRRFL	53						
Hsa MutY	51	CDGLARPEEWLQASVSSYHLFRDAEVTAFRGSELSDOE-KRDEIRRAEDMDLD		RRAYAVWVSEVMLLQTOVATVINYTGMM	139						
Spo MutY	1	MSDSNHFLDLHSYTQLEVERFESQFQXT-KRIEPRKKECIPPSSESPLEMEOPVORLYEVLSEIMLQOTRVEVTKRYTKMM			88						
Eco MutY	1	MOASQFSAQVLDWIDKYGRKTEPQ	ID	KTPYKVMISEVMLQOTQVATVIPPYFERFM	56						
Eco EndoIII	1	MNAKRLKTLREN	NPHPTT	ELN	FSSPFELLTAVELSAQATDVSNKATAKLY	55					
Tth MutY	54	ERFPTKALAAASIE-EVLRYWOGAGYYR-RAEHLHRLRSVEEL	PPSFAELR-GLPGLGPTYAAVAASHAFGERVAAY	GNVRRVLSRLFARES	145						
Hsa MutY	140	QKNGTODLSASIE-EVNOELAGLGYYS-EGRRLOEGARKVVEELGGHMPRTAETEOQLPGVGRYTAGATASIAFGQATGVV		GNVARVLCRVRAIGA	237						
Spo MutY	89	ETLPTKSCAEAYNTQVMPHSGMGFTY-CKRCHQAGHAKLHPSEIPRTGDEMAKGLPGVGPYTAGAVLSIAWIKOPTGIV		GNVIRVLSRALAHS	187						
Eco MutY	57	AREPTVTDLANAPED-EVLHHTGLGYA-BARNEHKAQOVATLHGKFPETFEVVA-ALPGVGRSTAGATLSLSLGKHFPIL		GNVKRVLAACYAVSG	153						
Eco EndoIII	56	PVANTPAAMLELGYE-GVKTYIKTIGLYNSKAENLIKTERILLEHNGEVPEDRAALE-ALPGVGRKTANWALNTAFGMPTIAV		THIFRVCNRTQFAPG	153						
Tth MutY	146	-PK-EKEEFALAGGLPEGVDPGVWNOALNELGATVCLPKPRCGACPGAFCRG	KEAPGRYP	APR	K	210					
Hsa MutY	238	DPSSTLYSQOHWGLAQQVDP-ARPGDINQAWNELGATVCTPORPLCSQDVESLCRARORVEQEOQLASGSLSGSPDVEECAPNTGQCHCLPSPSEPD				336					
Spo MutY	188	DCSKGKANALNKKANELVDP-VRPGDENQALNELGATCTPQSPRSCVQISEICKAYO	EQNVIRGNTIKYD	IEDVPCN-ICITDIPS	K	276					
Eco MutY	154	WPGKKEVENKMSSEQVTPA-VGVERENQAMMDIGAMICTRSPKPKSLCPQONGCIA	AANNSWALYP	GKK	P	225					
Eco EndoIII	154	KN-VEQVEEKLKVPVPA-EFKYDCHEMLLHGRTYCIRKPRCGSCILEDLCEY				205					
Tth MutY	211	RRAK	EER-LVALVLLGRKG	VHLREGR	FOGLYGVLPFP	EELP	GREAFGVRS	RP	L	266	
Hsa MutY	337	OTLGV	VNFRKASRKPPRESSATCVLEPGA	LGQIIL	YVORPNSQILAGLMEEPSVTW	EP	SEOLORKALLLOELORWAGP		LPATHLRHL	425	
Spo MutY	277	EDLQNVVARYPVHPAKTKORE-ERALVVFQKTDPSKKEFLIRKPSAGLLAGLWDEPTIEFGQESWPKMDMAEFQKSIQDWISNDRSLIKKYQSR								375	
Eco MutY	226	OTL	PER	TGYFLLLOH	EDEVLAQDPPSQWGLYCEPQFAD	EES			LROMLAQRQ	IADNLTOL	287
Eco EndoIII	206	K				EKVDI					
Tth MutY	267	GEVRHALTHRLR	VEVR-GALWEGEDDPWKR	LPKLMKVLRLALP			PLAH		AGWPLPDA	325	
Hsa MutY	426	GEWHTESHIKLTYQVYGLAEGOTPVTTVPPGAPMLTOEFTHTAAVSTAMKKVFRVYQGOQGTGCMGSKRSOVSS							CSRRKPRMGQOVLDNFFRSHISTDAHSLNSAAQ	535	
Spo MutY	376	GRYLHIESHIRKTSHFYAIAS	PDIVTNEDEFFISQDLHVGMC	ELGLKNRAALEIKRK			VTSLN		FKEPKLTSARRIVTKAEC461		
Eco MutY	288	TAFRTESHFHD	IYP	MMLPVSSFTGMD	EGNALWYLNLAQ	PSVG	LAAPVER		LLOOLRTGAPV	350	

Tth (*Thermus thermophilus* HB8), Hsa (*Homo sapiens*), Spo (*Schizosaccharomyces pombe*), Eco (*Escherichia coli*)

Residue essential for N-glycosylase activity * Residues constituting an iron-sulfur cluster (D)

Fig.6

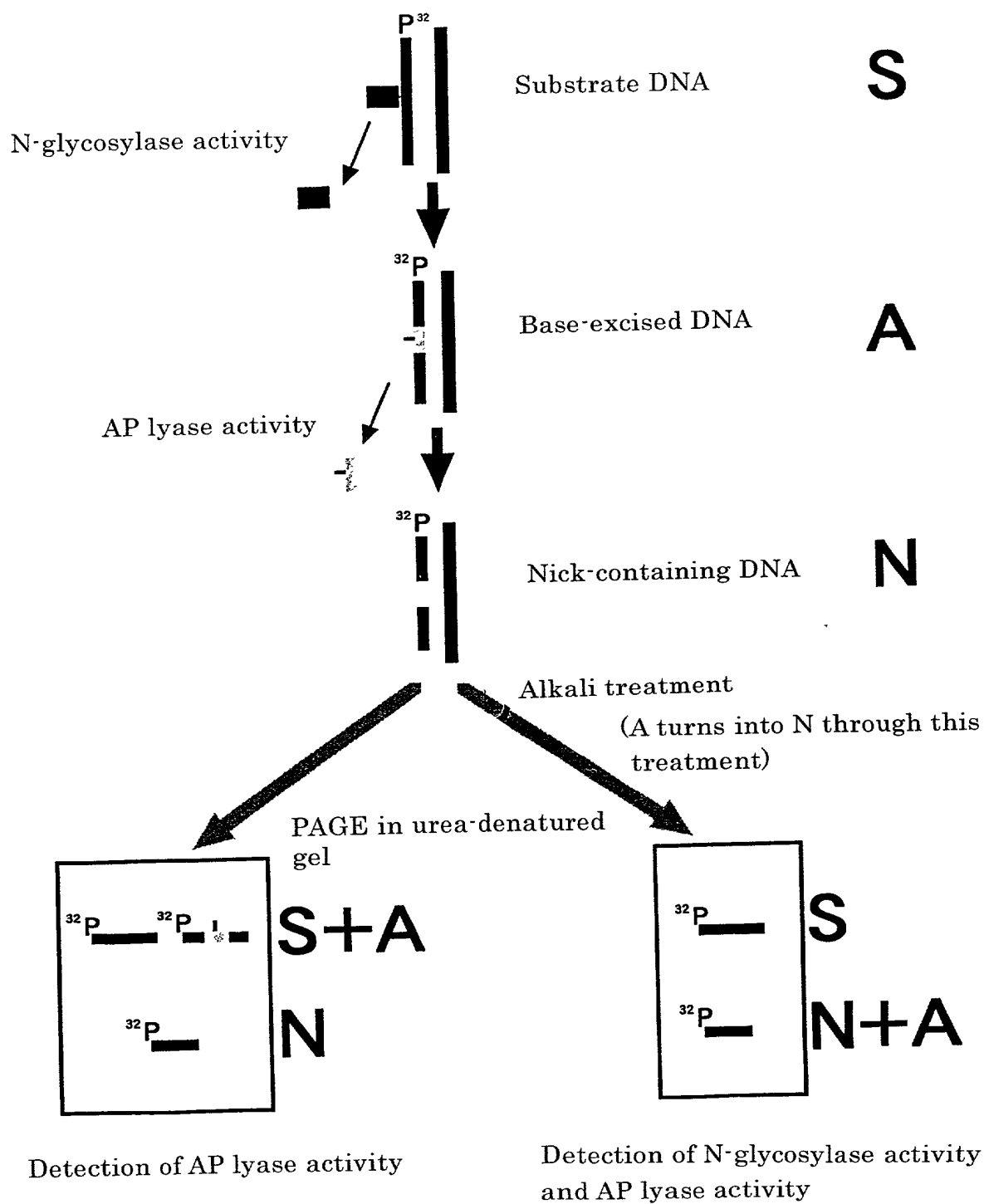


Fig.7

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21



Fig.8

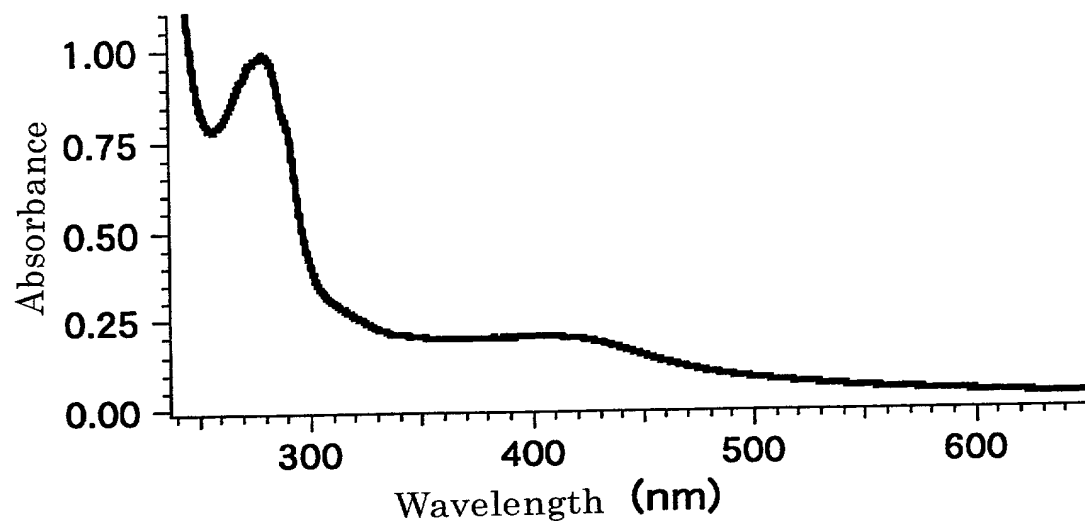


Fig.9

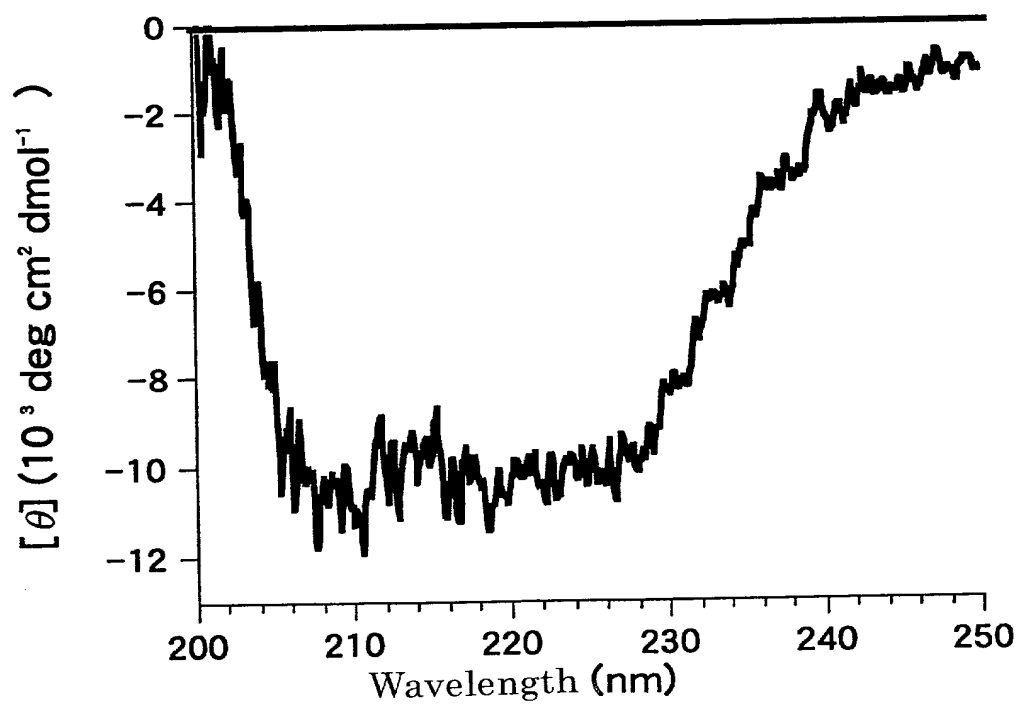


Fig.10

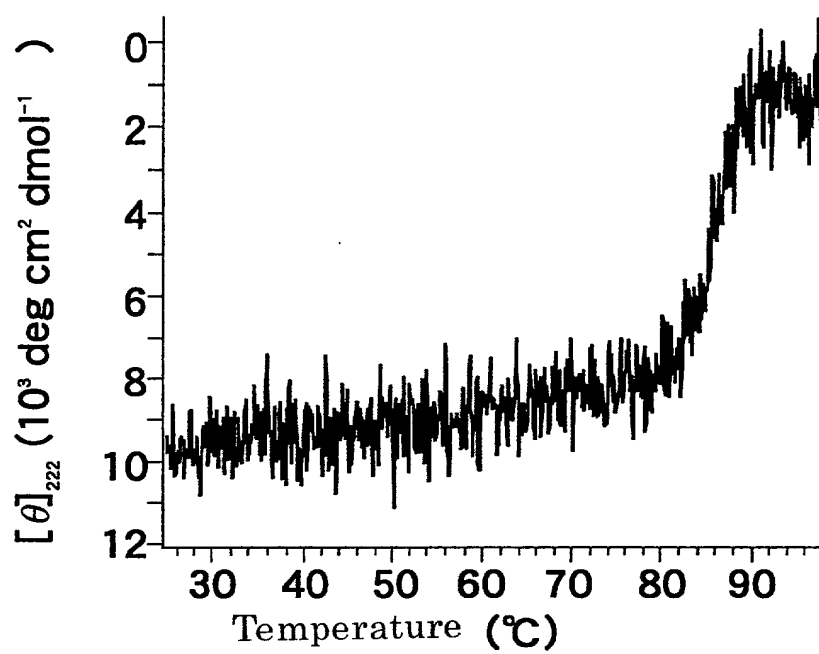


Fig.11

5' - [32P] AGATCTTGACGGGGAAAYCCGAATTCGGCGAACGTGGCGAG - 3'
 3' - AATCTAGAACTGCCCCTTTXGGCTTAAGCCGCTTGCACCGCTCTT - 5'

X : G, G, C, T

Y : A, G



Annealing

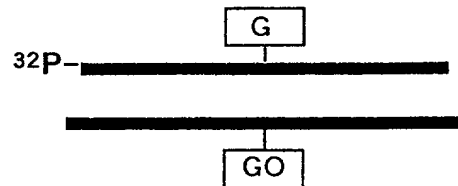
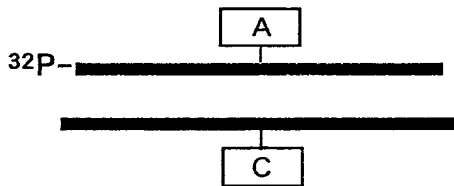
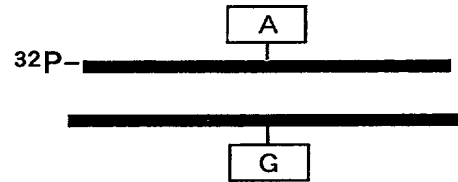
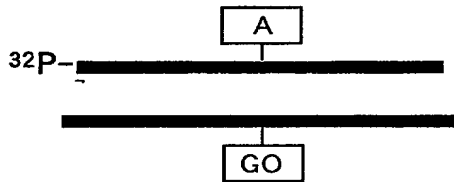


Fig.12

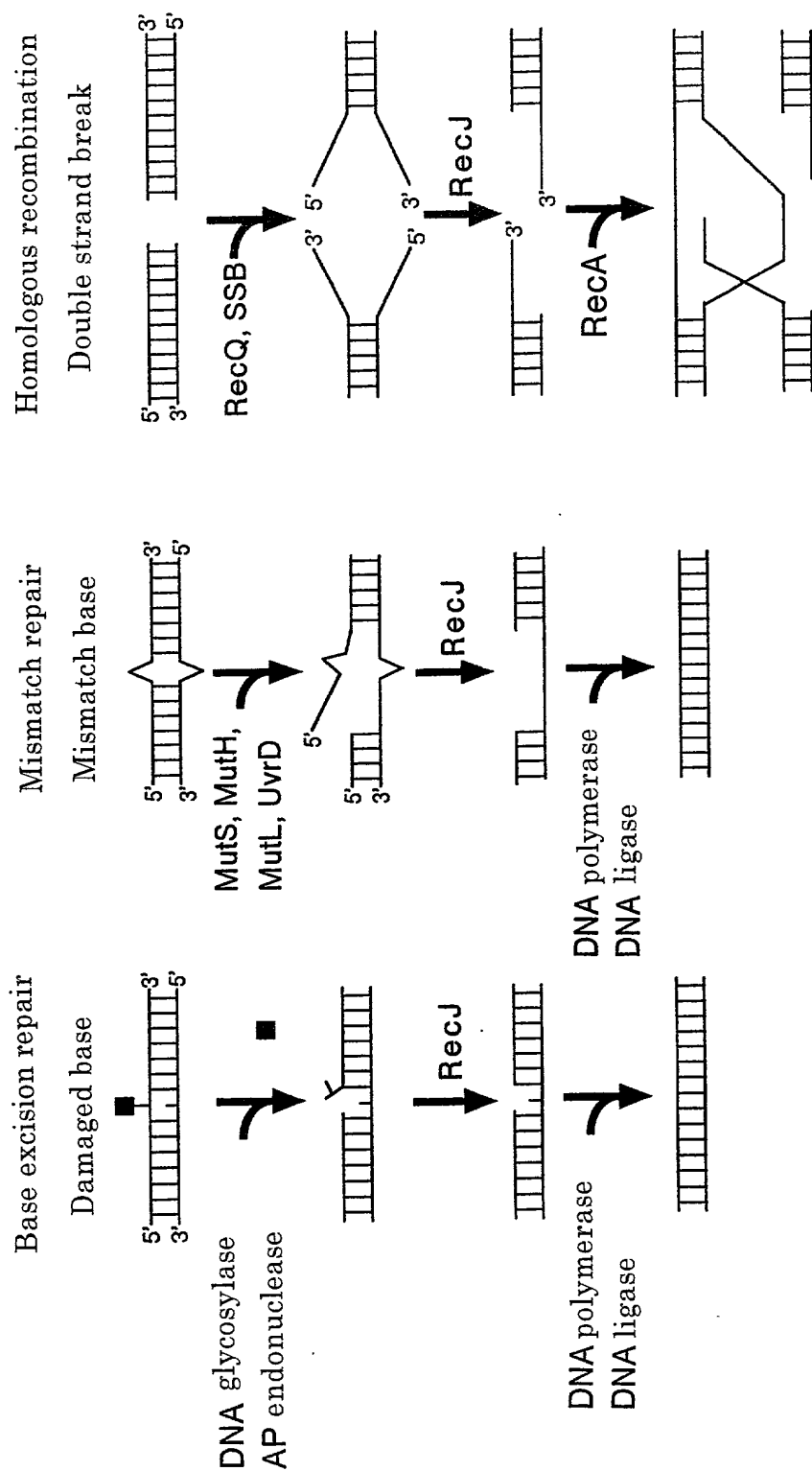


Fig.13

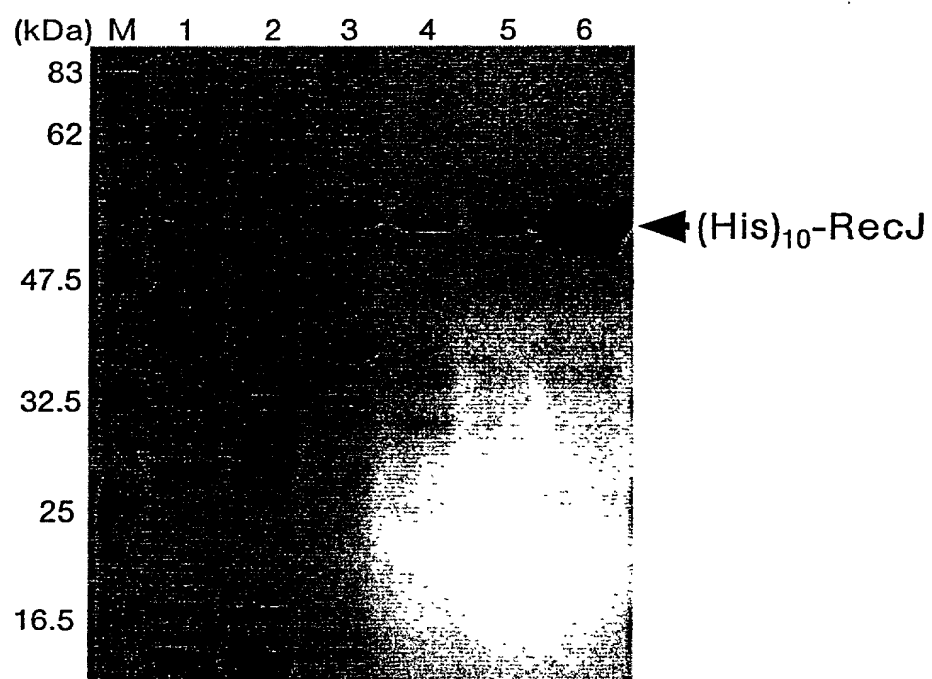


Fig.14

Motif I

RecJ_Tt	[73]	KRIRVHG DY A S G L T G T A I L V R G L A A L G	[100]
RecJ_Ec	[73]	TRIIIVG D F A A G A T S T A L S V L A M R S L G	[100]
RecJ_Aa	[56]	KRIIIYG D Y V G I T G T A I L Y R V L K L L G	[79]
RecJ_Hp	[47]	TEILVVG D Y A G V I S S A I M A K F F E S L N	[74]
RecJ_Hi	[67]	QKIVIVG D F A A G A T S T A L S V L A L R Q L G	[90]
PPX1_Sc	[29]	TICVGNESA M S I A S A T T Y S Y C Q Y I Y N	[52]
PRUNE_Dm	[37]	HLVMGNESC L S A V S A V T L A F V Y A A S S	[60]

Motif II

RecJ_Tt	[128]	SDL F L T V C G I T N H A E L R E	[147]
RecJ_Ec	[131]	AQL I V T V N G I S S H A G V E H	[150]
RecJ_Aa	[133]	GDF L T V N G T S A V E E I D Q	[152]
RecJ_Hp	[102]	APL I T V N G I N A F E A A R F	[121]
RecJ_Hi	[126]	VQL L M T V N G V S S F D G V A F	[145]
PPX1_Sc	[120]	ELNSY L V N N D T P K N L K N Y	[139]
PRUNE_Dm	[87]	PLV G E M V C R A R V A L P R R Y	[106]

Motif III

[153]	VEV I V T P G K	[165]
[155]	IPV I V T L P G D	[165]
[154]	LET V V I N V P P	[164]
[126]	YTL I E T C L H H	[136]
[150]	IRVLVT L P P E	[151]
[141]	NVVG T I F F D L Q	[153]
[128]	NVTEIL R P L E D	[140]

Motif IV

RecJ_Tt	[209]	YAD L A A V G T I A V A P L W G W	[228]
RecJ_Ec	[226]	LLD L V A L G T I A V V P L D A N	[245]
RecJ_Aa	[215]	FLD L V A L G L E A Y M P V N P V	[234]
RecJ_Hp	[189]	LLC L A G V A T I A M M P E T F F	[208]
RecJ_Hi	[219]	LLD L V A L G T I A V V P L D Q N	[238]
PPX1_Sc	[191]	I A L L M G A T I I T S N M R R K	[210]
PRUNE_Dm	[183]	V A Q L L H A T I V L T I N F A P A	[202]

Specific motif

[386]	D L L L R Y K E A A G F A M	[402]
[421]	G M M L K F A M A A G L S L	[438]
[404]	D M F L K W D K A M G L T L	[420]
[372]	S L L L G Y R Q A C G L S V	[388]
[415]	N M I L K F A M A A G L S I	[431]

Tt : *Thermus thermophilus* HB8, Ec : *Escherichia coli*, Aa : *Aquifex aeolicus*,
 Hp : *Helicobacter pyroli*, Hi : *Haemophilus influenzae* Rd,
 Sc : *Saccharomyces cerevisiae*, Dm : *Drosophila melanogaster*

Fig.15

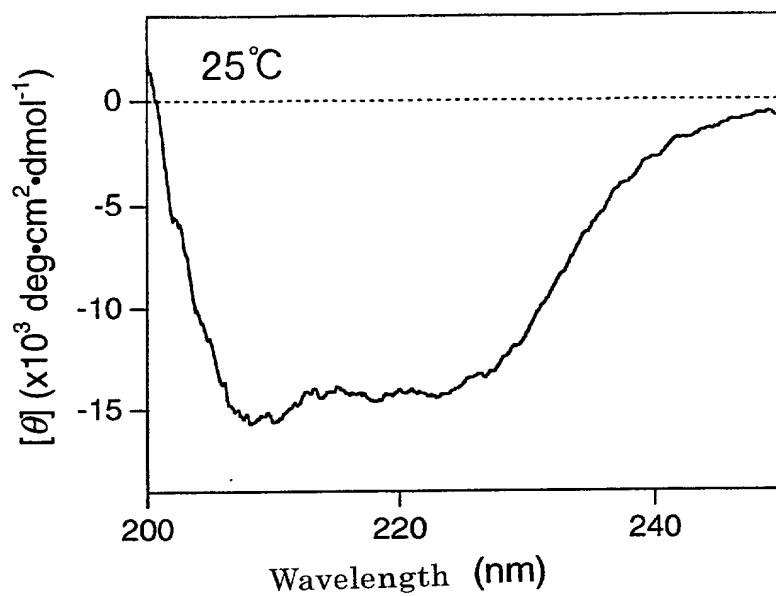


Fig.16

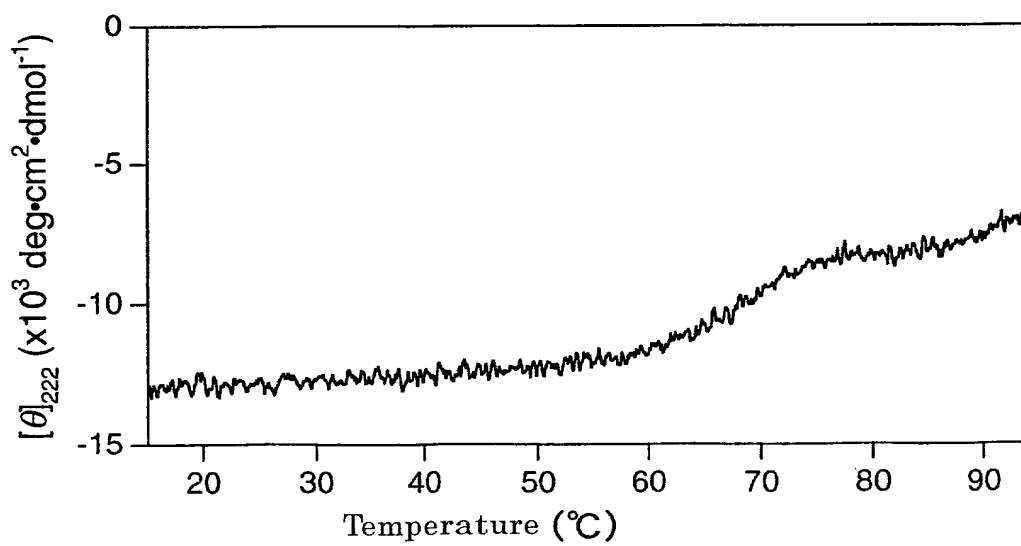


Fig.17

Substrate DNA : 49-mer ssDNA

5'-ACTACTTGGTACACTGACGCGAGCACGCAGGAGCTCATTCCAGTGCGCA-3'

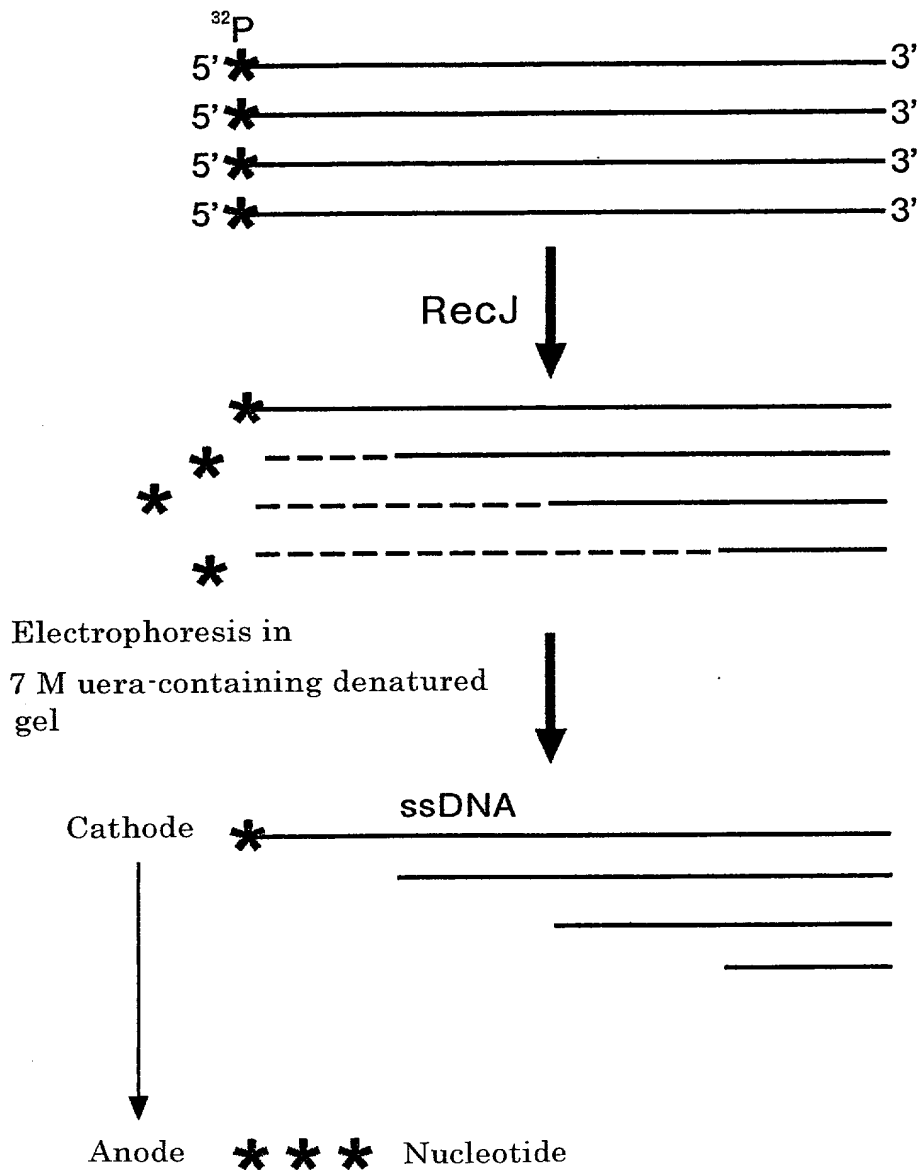


Fig.18

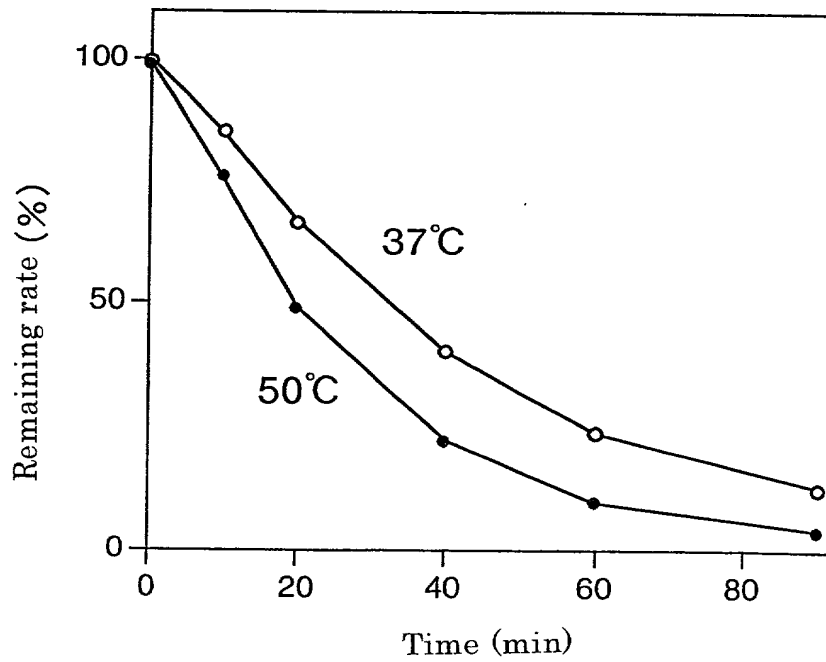
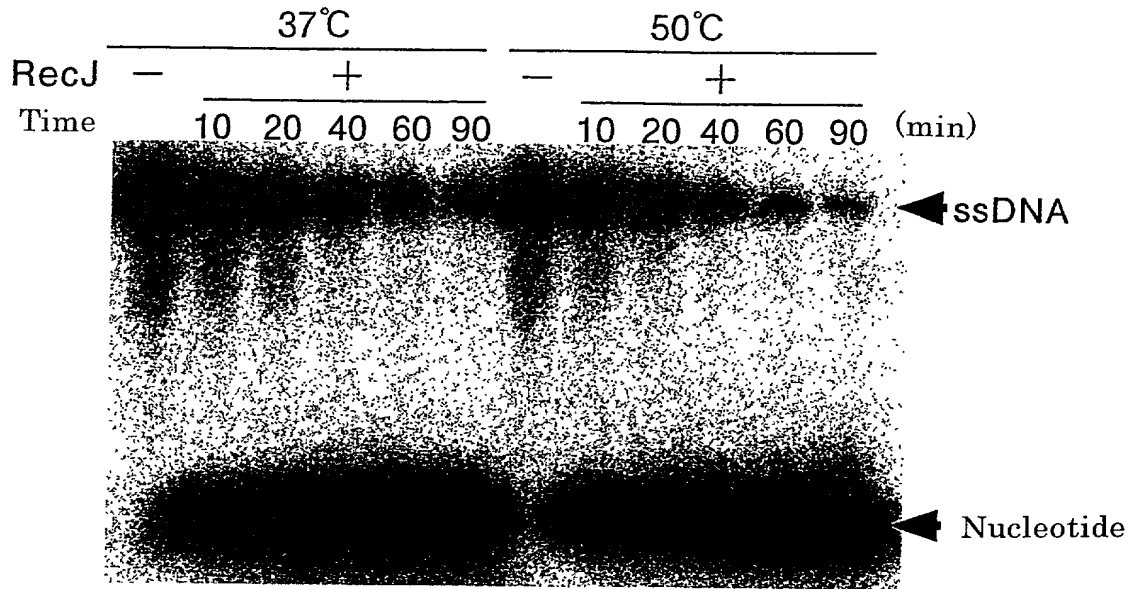


Fig.19

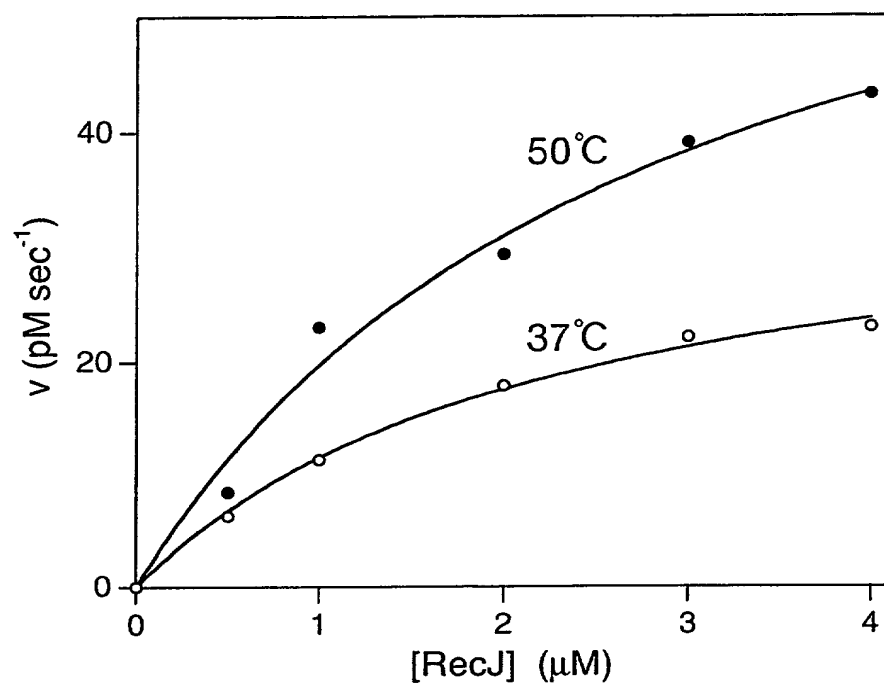


Fig.20

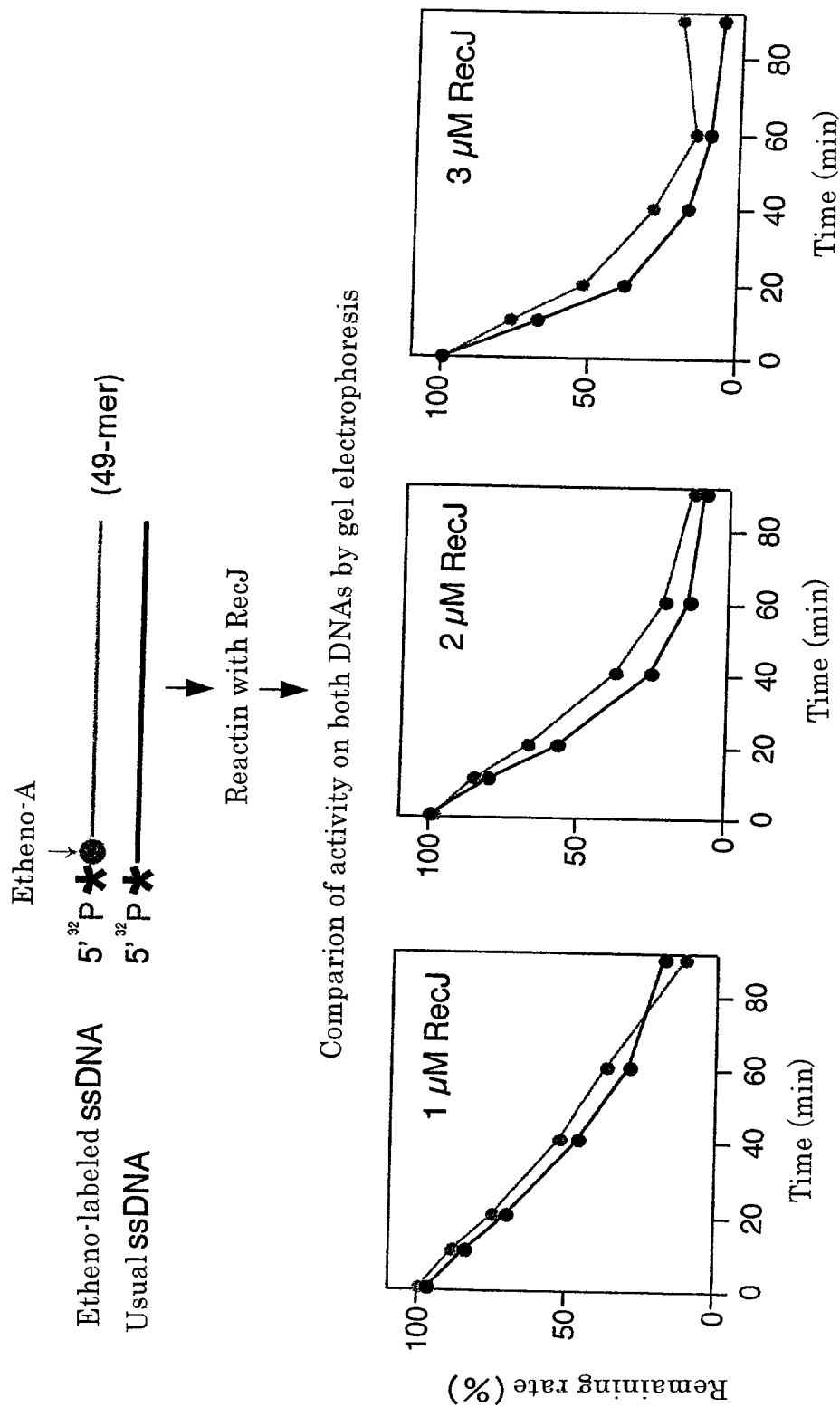
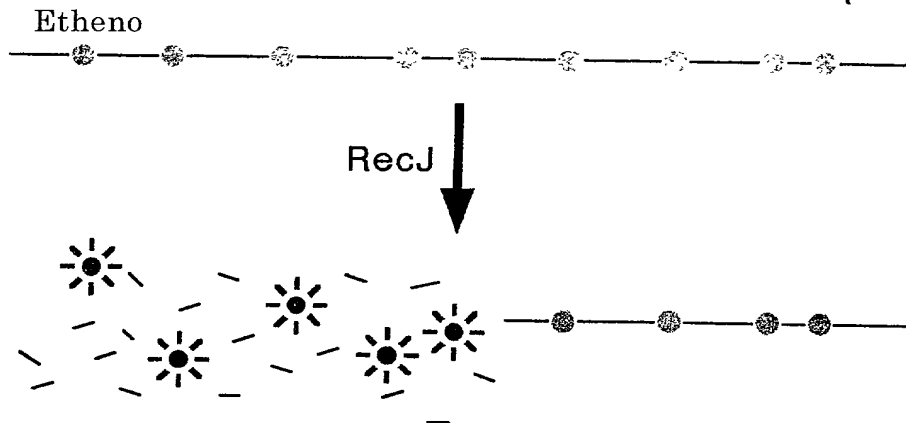


Fig.21

Substrate DNA : Etheno-labeled bovine thymus ssDNA (ϵ DNA)



Fluorescence Spectrum

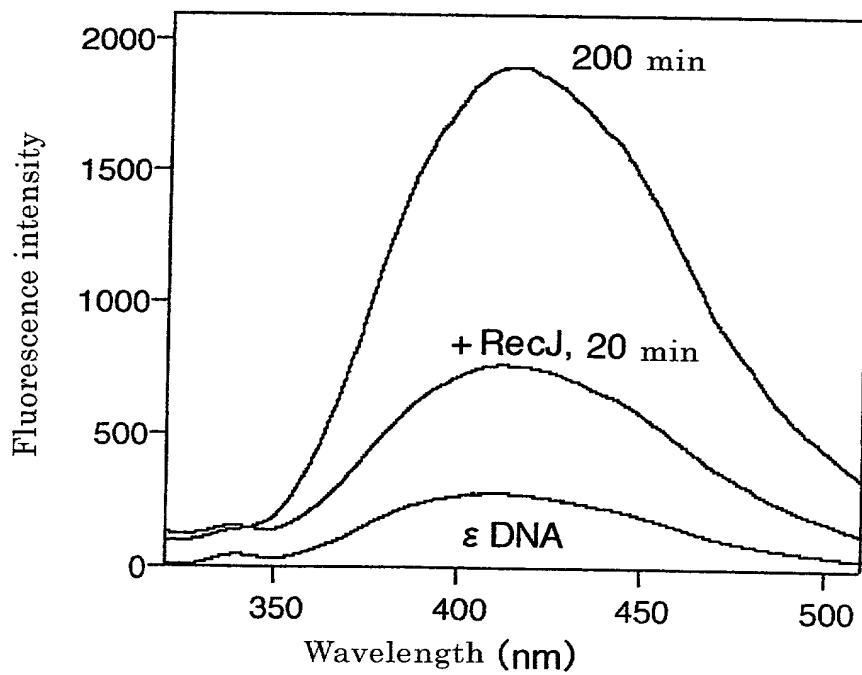


Fig.22

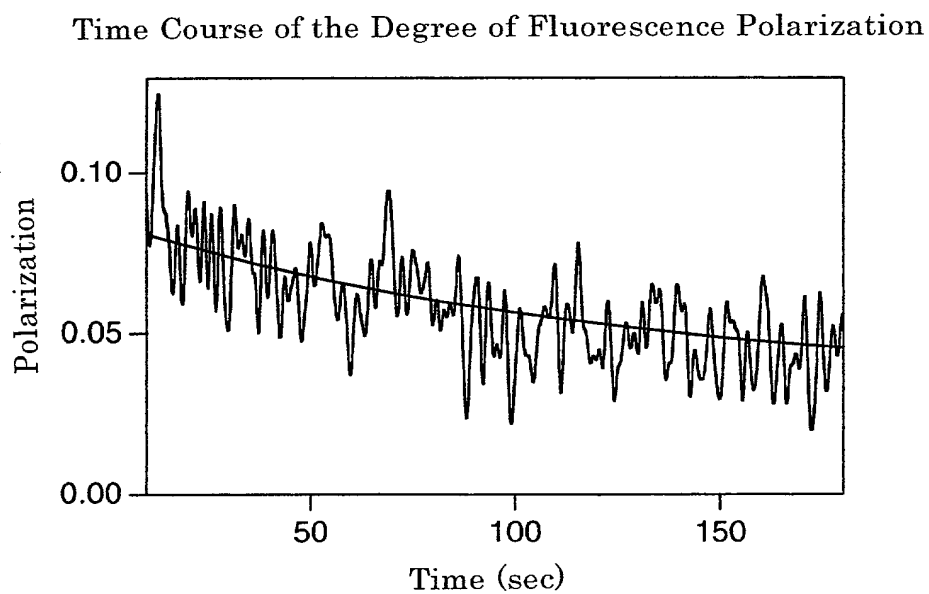
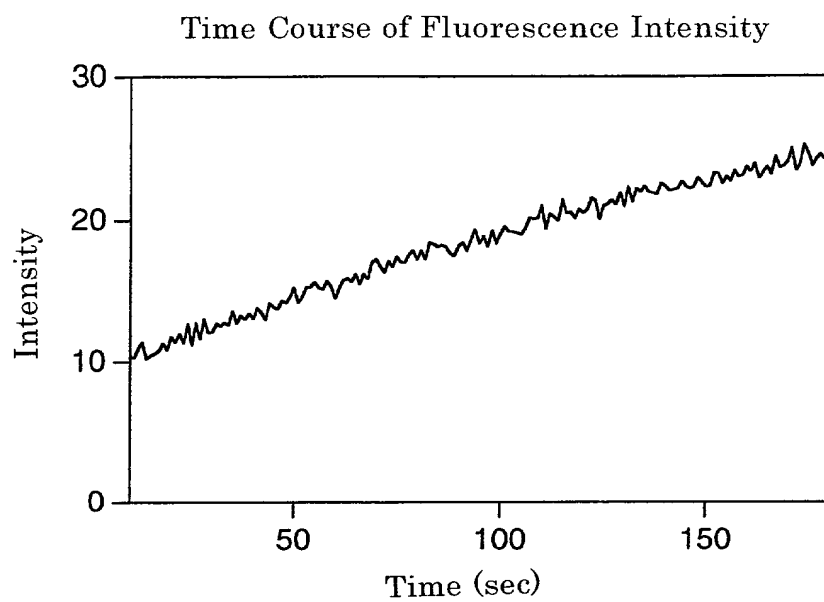


Fig.23

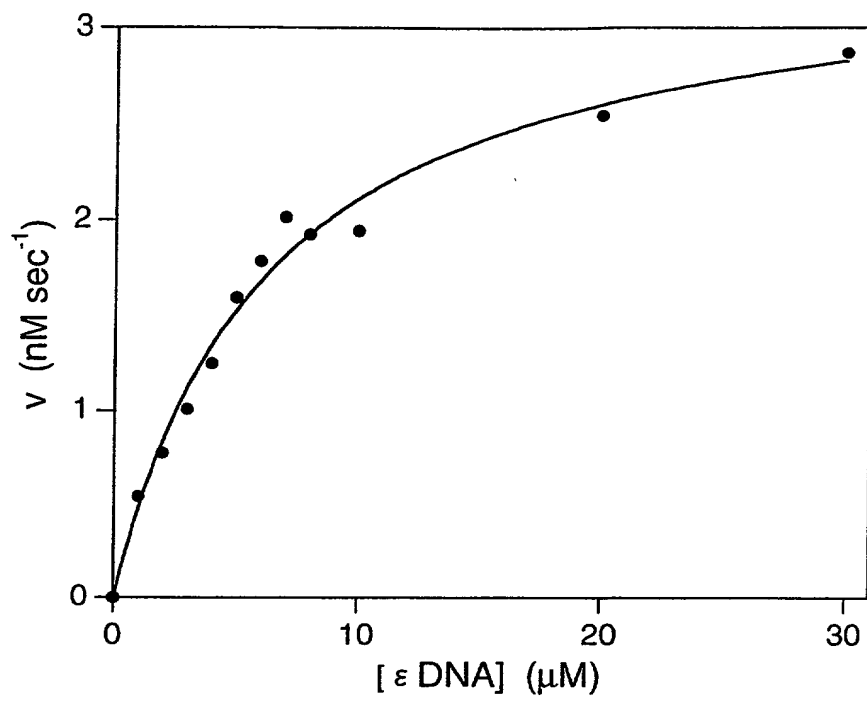


Fig.24

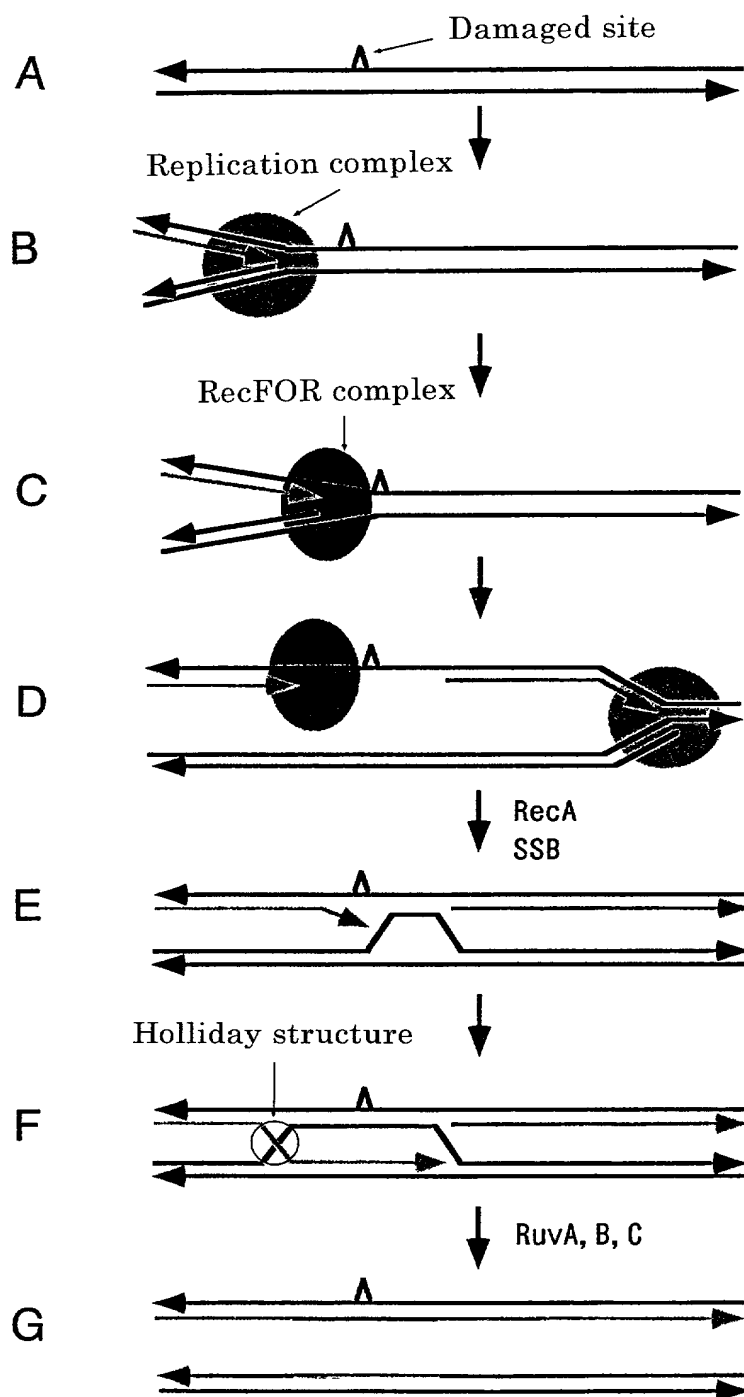


Fig.25

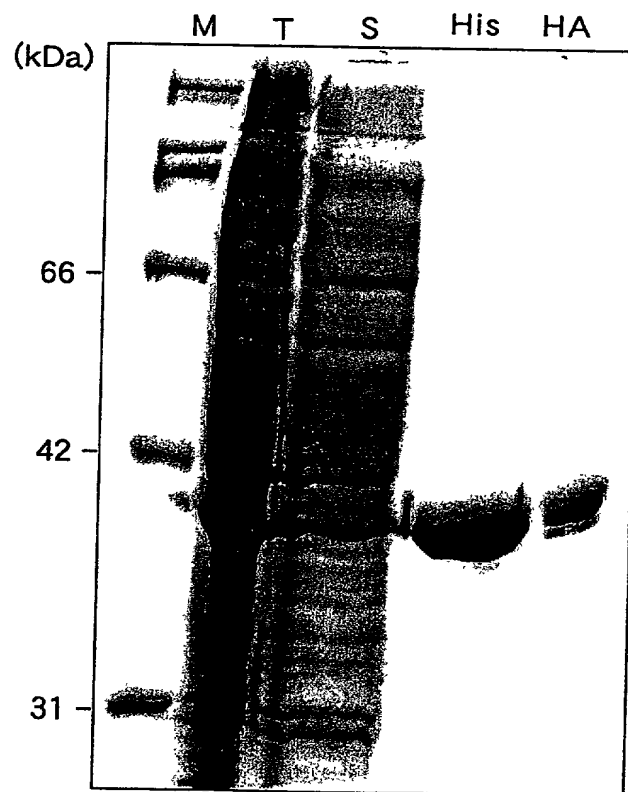


Fig.26

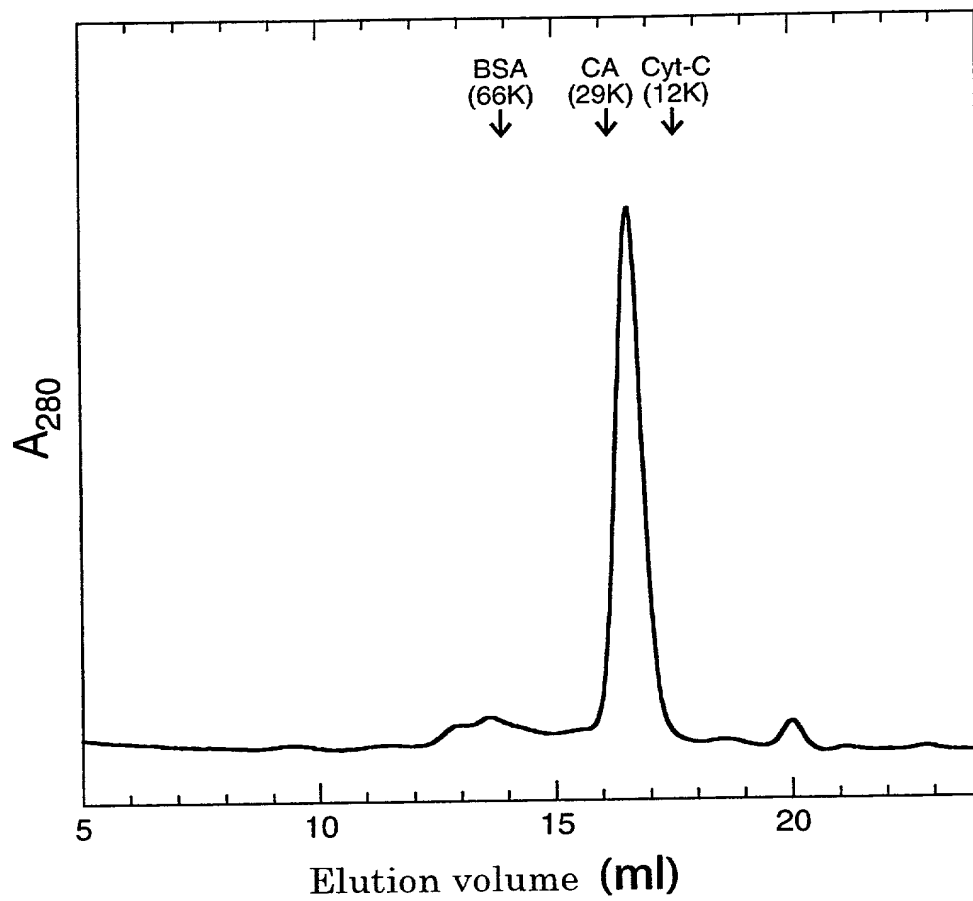


Fig.28

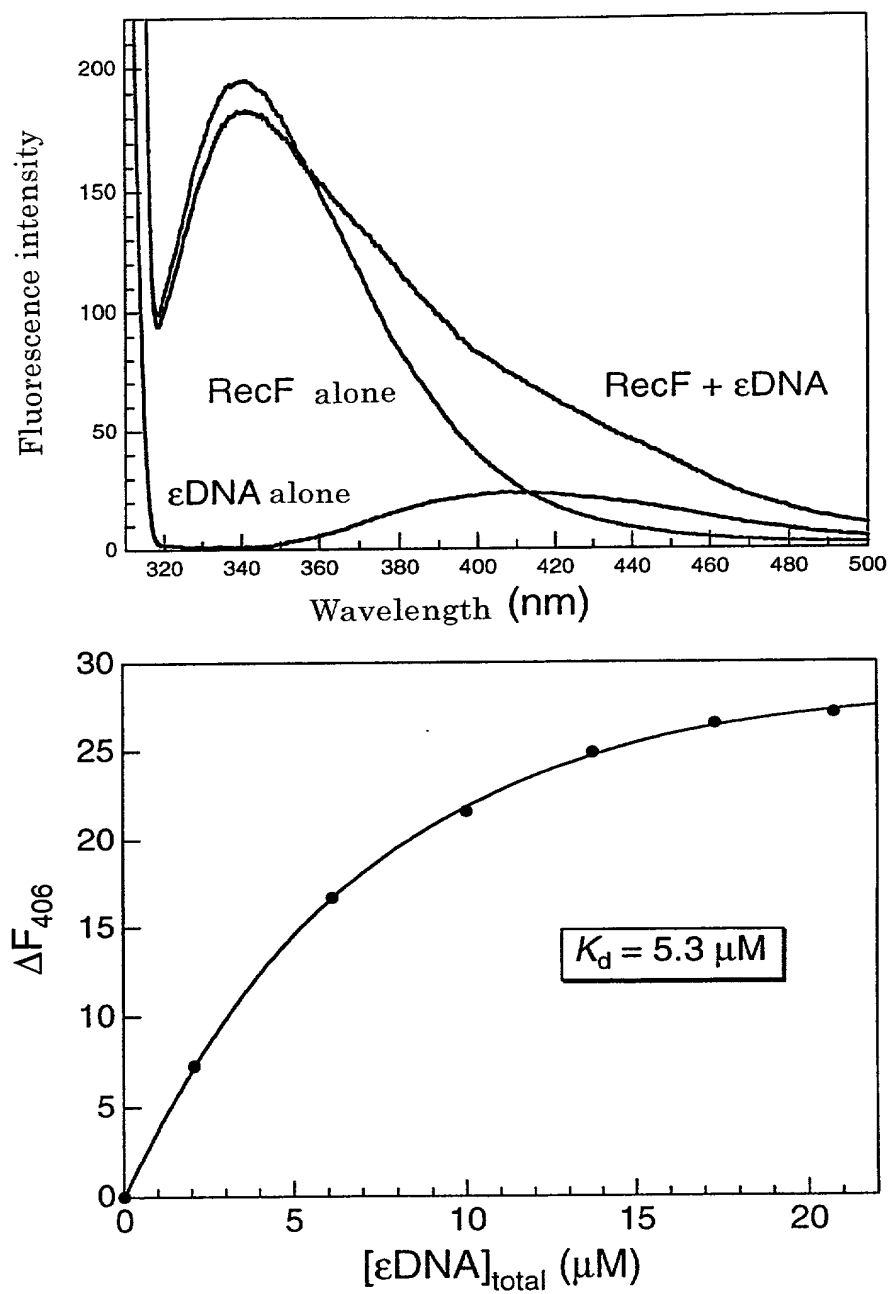


Fig.29

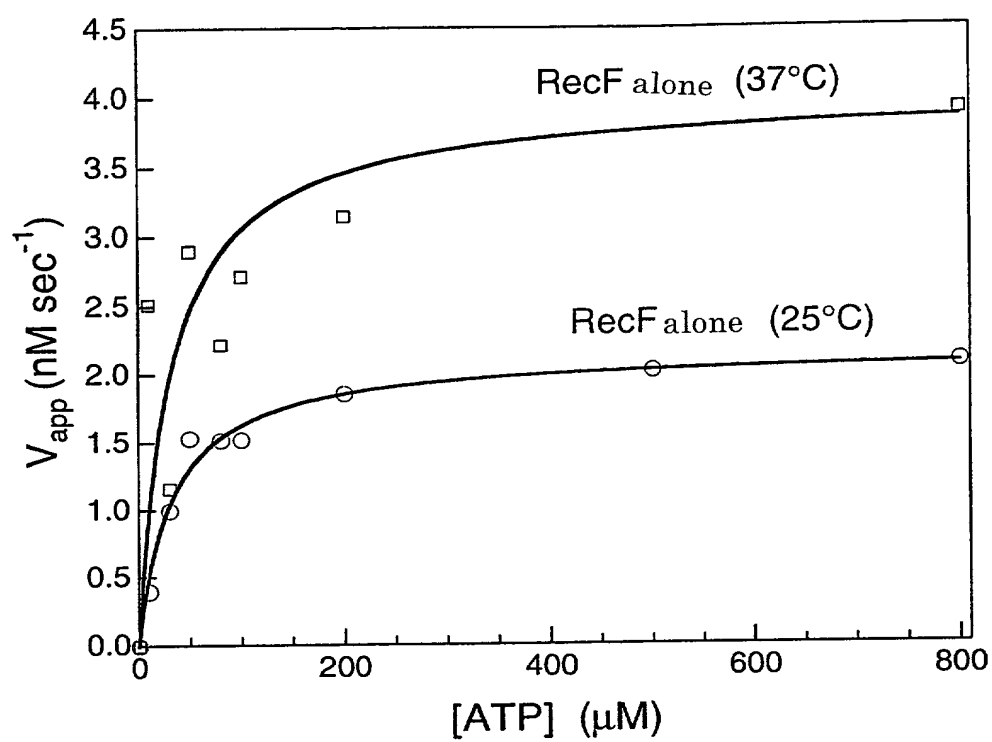


Fig.30

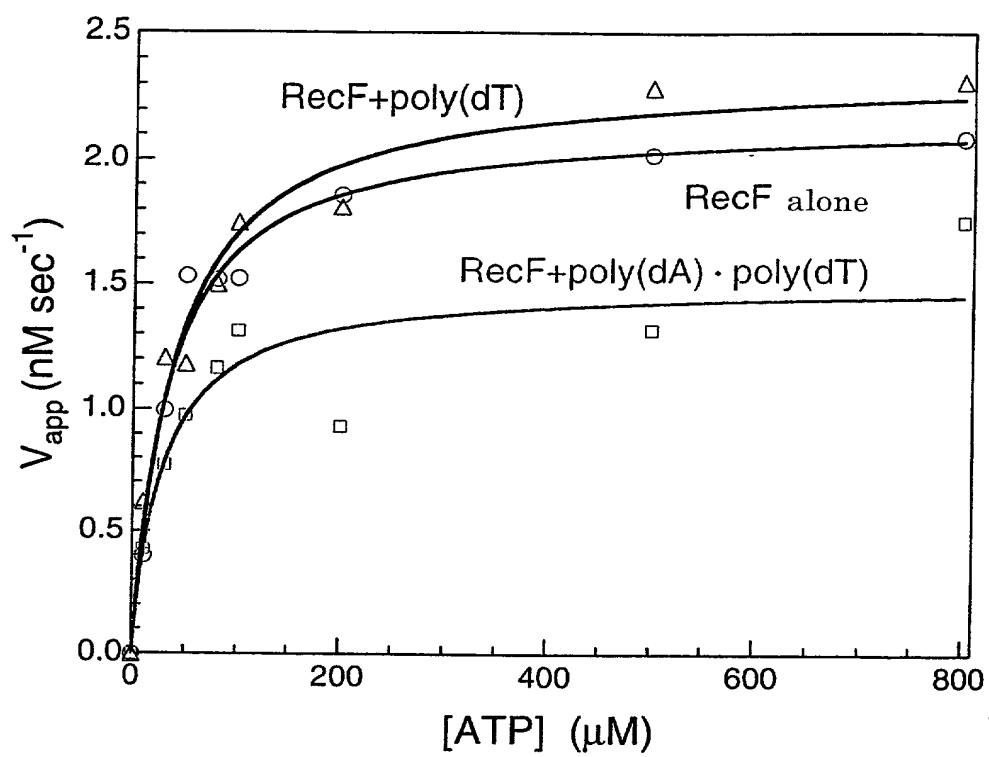


Fig.31

Repair of Entire Genome

Transcription-Coupled Repair

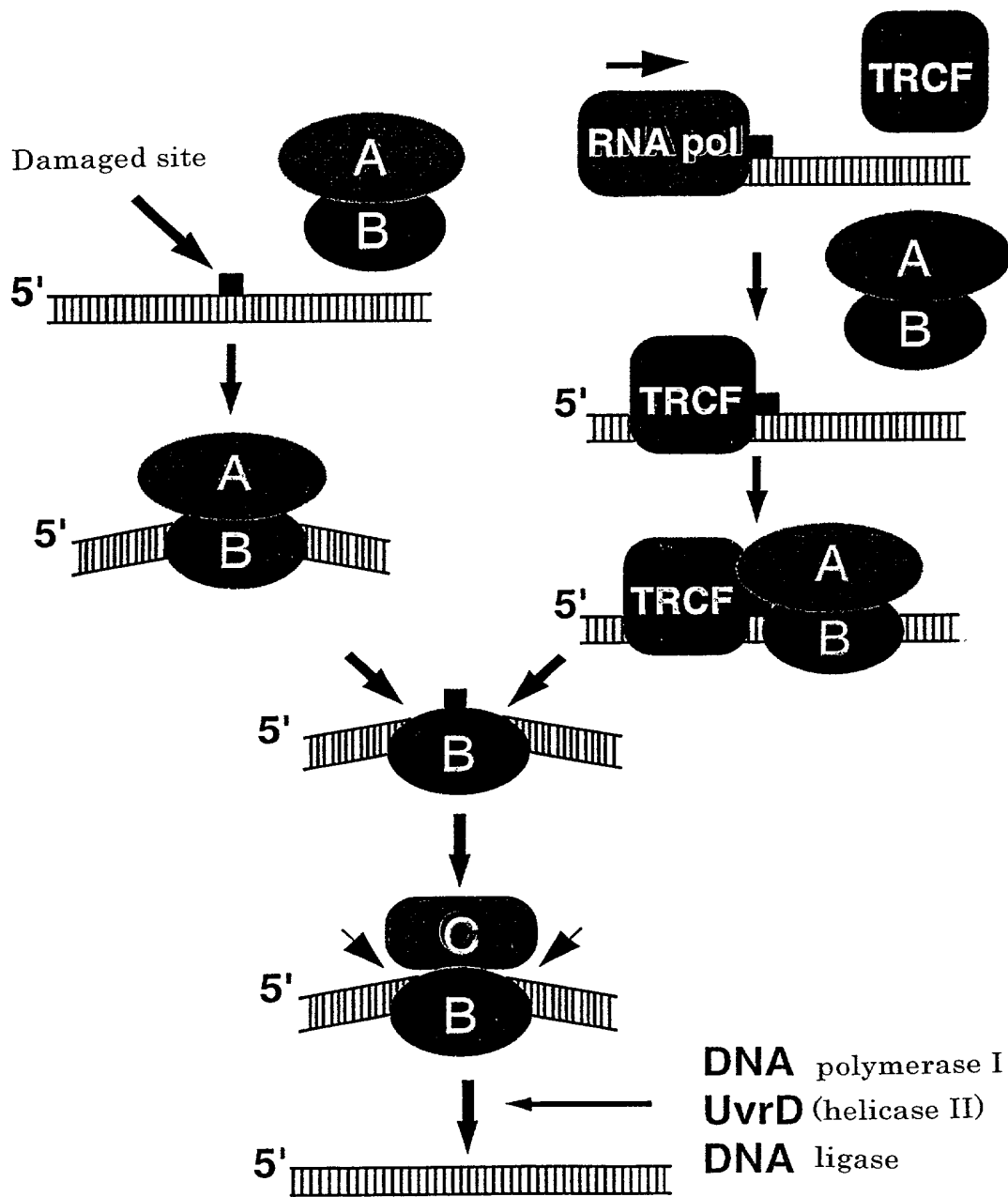


Fig.32

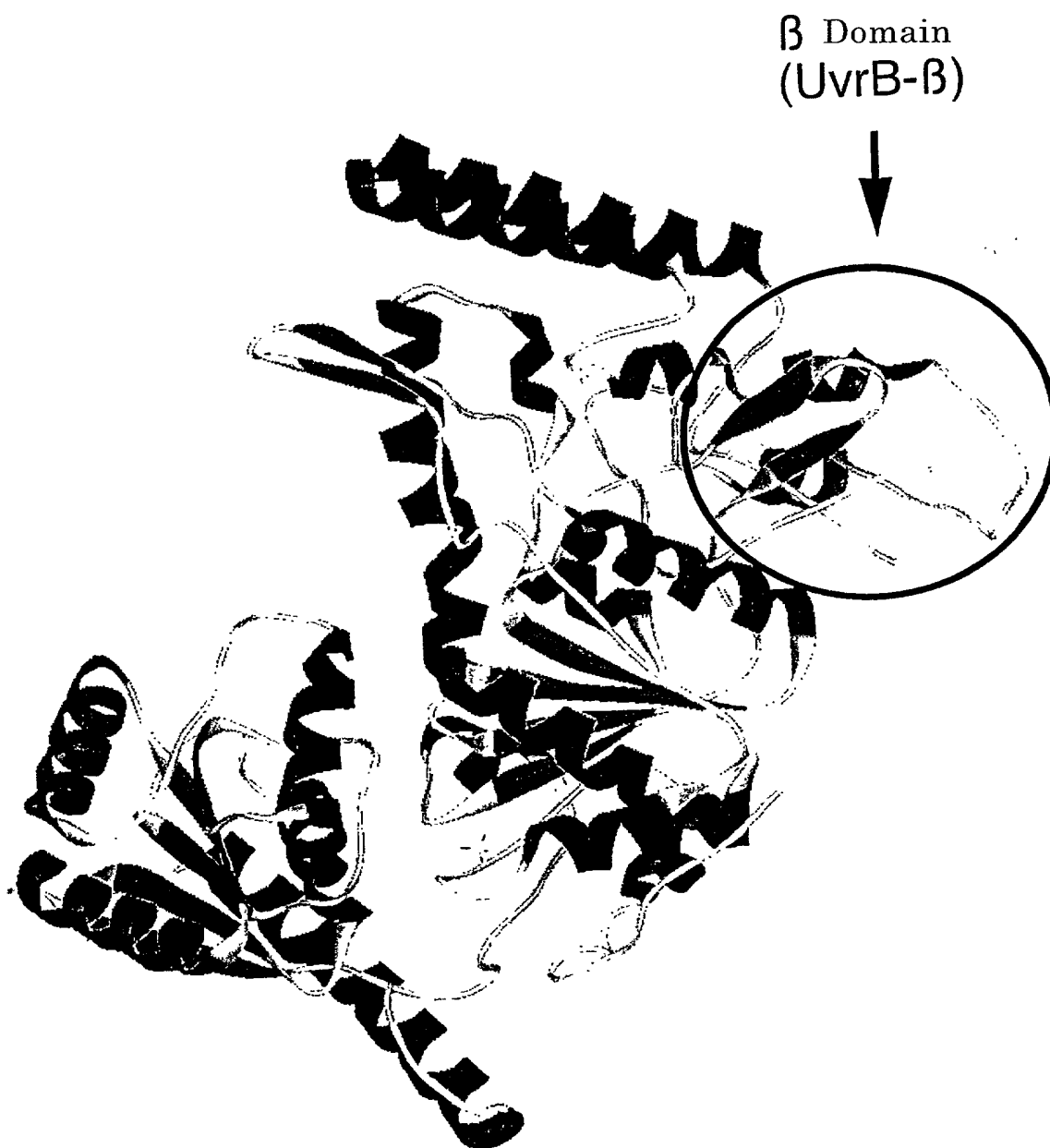
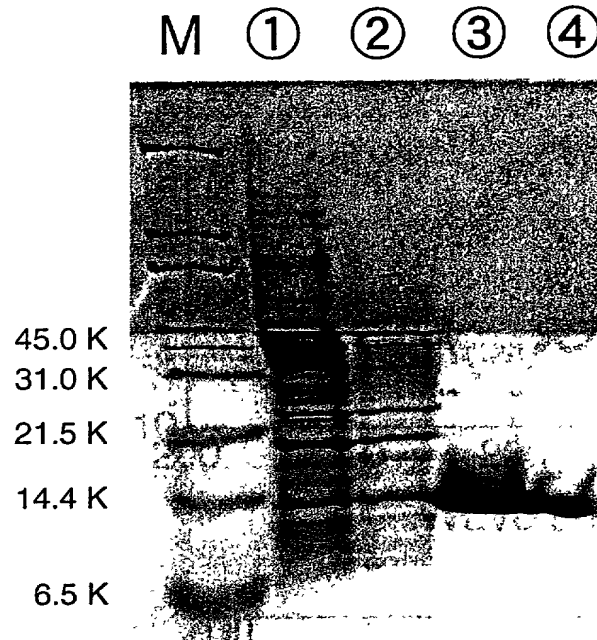


Fig.33

UvrB- β



TRCF- β

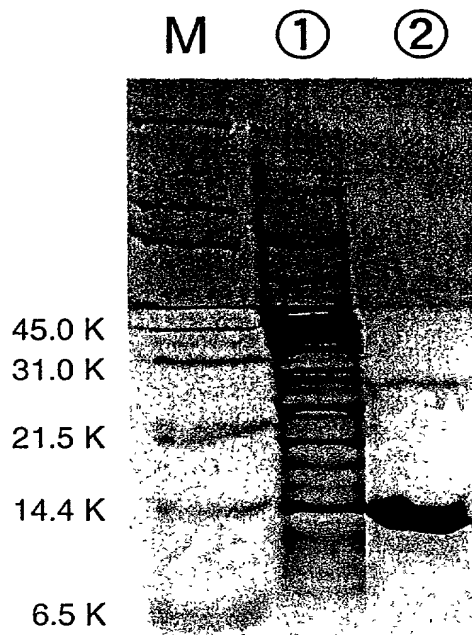


Fig.34

UvrB-β 154 RNLVVERGKPYPREVLLERLLELGYQRNDI 184
 TRCF-β 86 WRLLLEVGRAYPREALLSRLLKLGYAR--- 113

* . . * * . * * * * * * * * * *

UvrB-β 185 DLSPGRFRAKGEVLEIFPAYETEPTRVELF 215
 TRCF-β 114 DED---YRVLGEVVELG-----EVRLEFF 148

* . * * * * . * . * *

UvrB-β 216 GDEVERISQVHPVTG-ERLRELPG----- 236
 TRCF-β 149 GDELERLVVRGEERRRHVLLPKPGKAEGFT 163

* * * * * * *

UvrB-β 237 ---FVL FPA 242
 TRCF-β 164 SKKVLHEPG 172

. **

* Identical amino acid residues

. Homologous amino acid residues

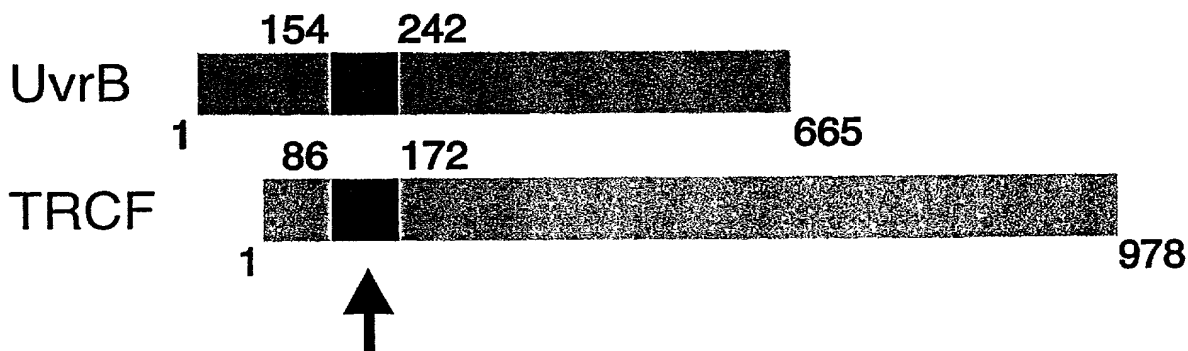


Fig.35

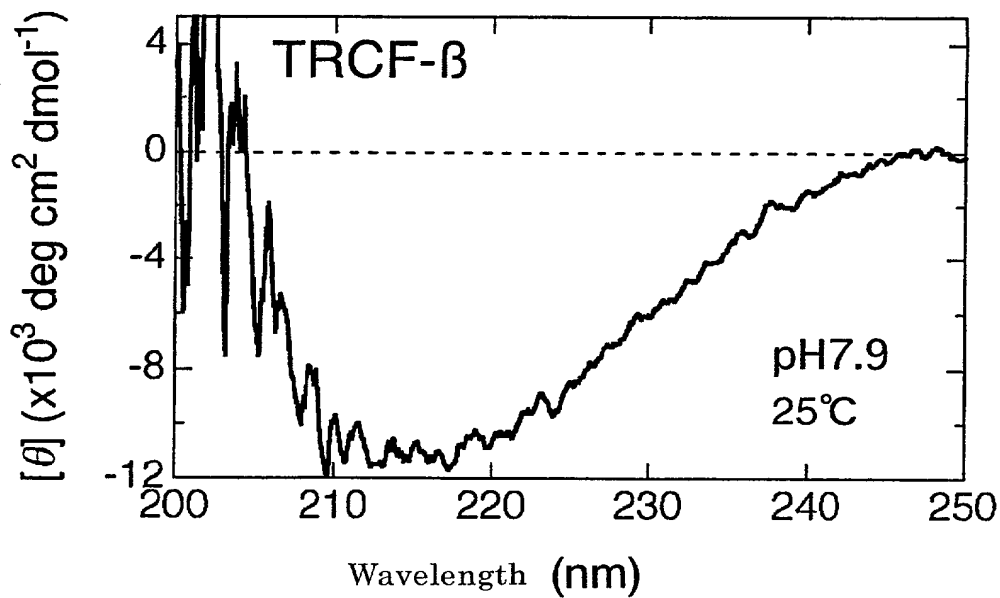
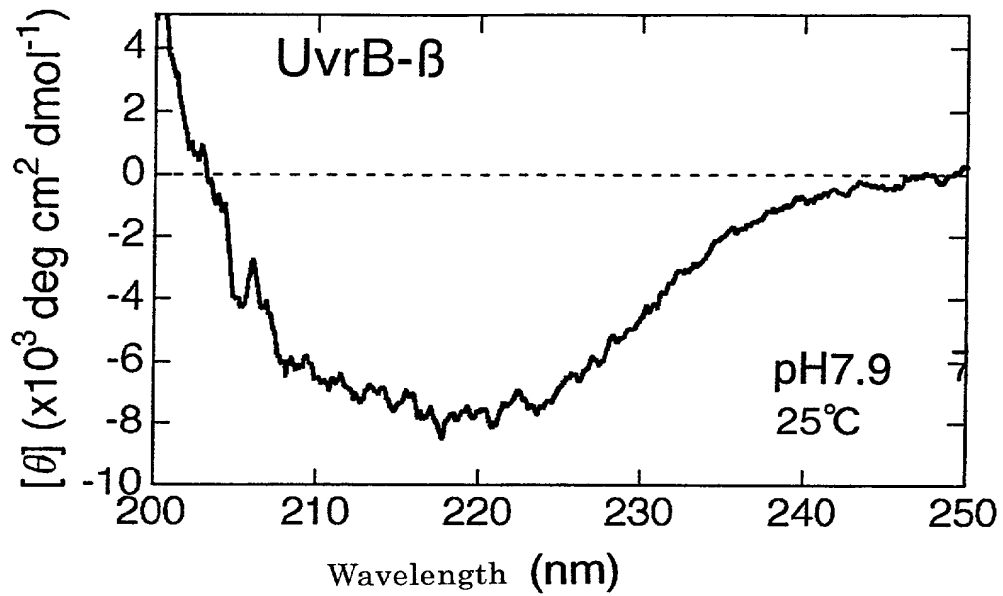


Fig.36

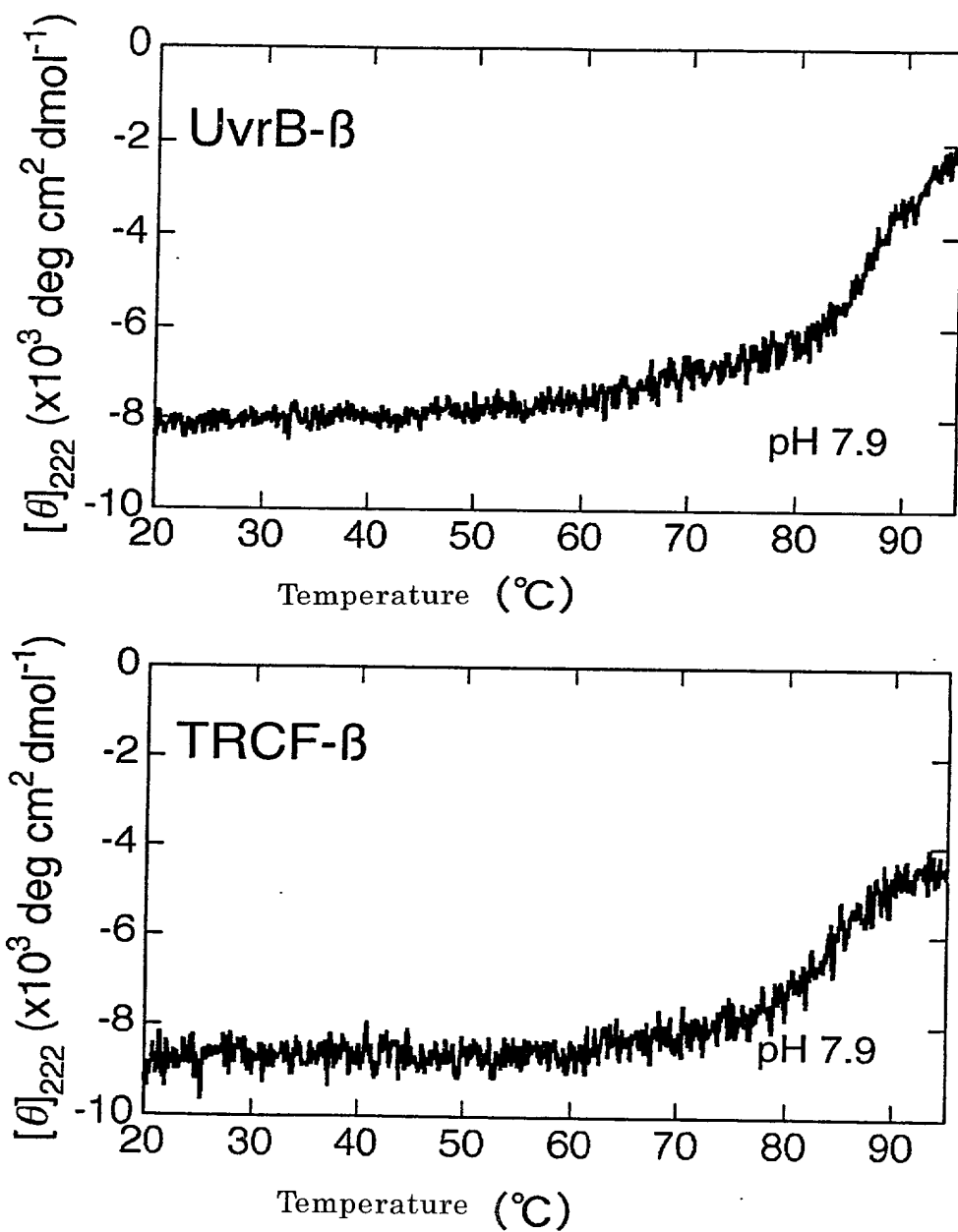


Fig.37

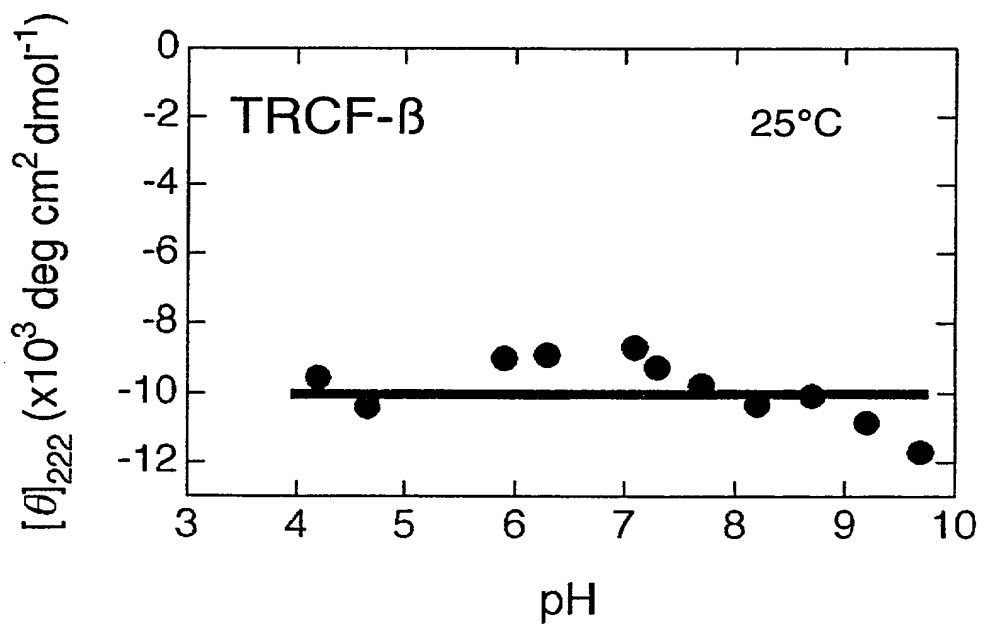
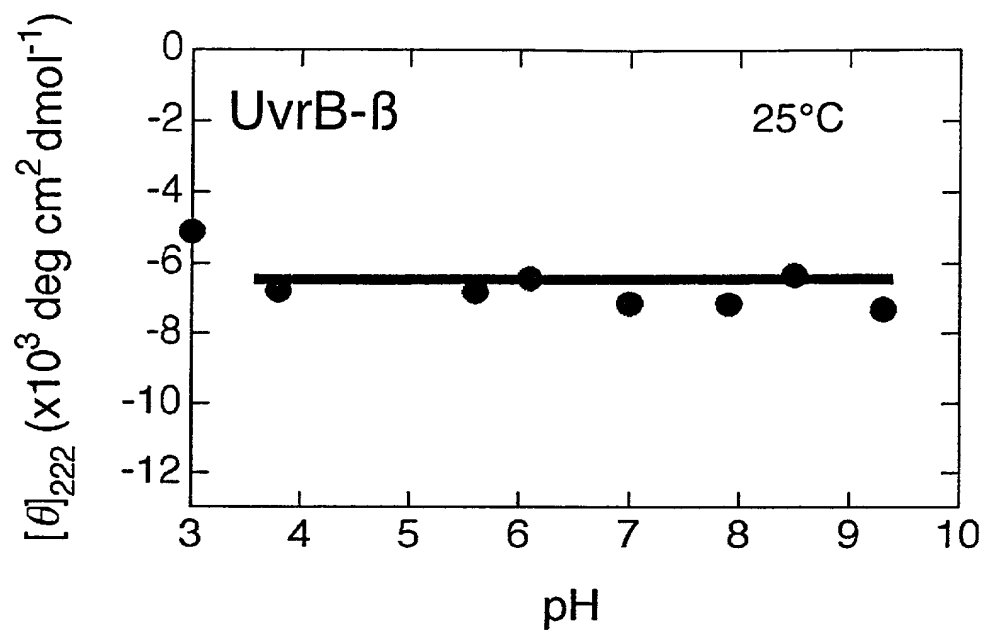


Fig.38

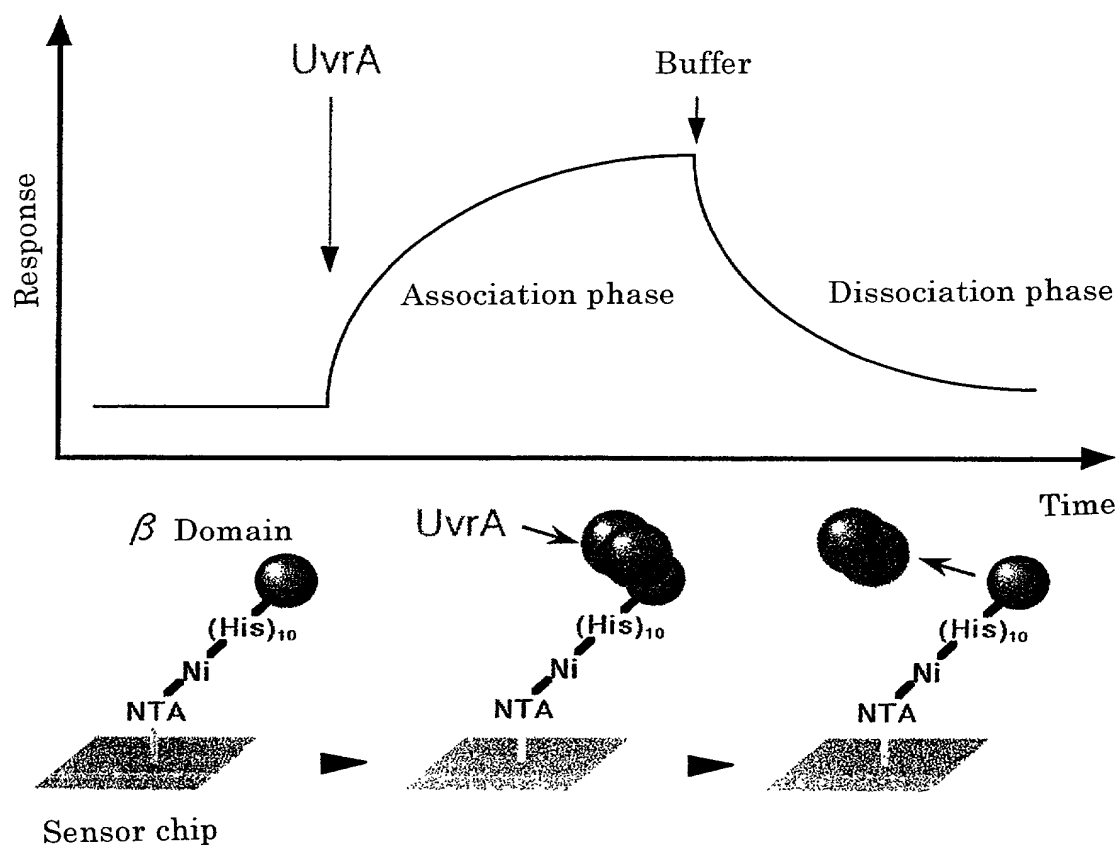
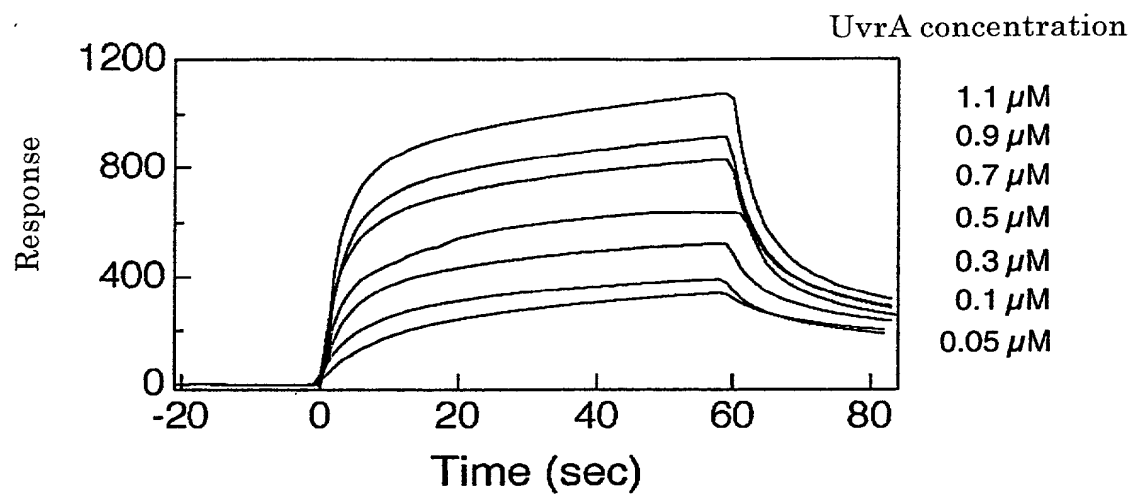


Fig.39

Sensorgram



Analytical Results

	K_d ($\times 10^{-6}$ M)		k_{on} ($\times 10^5$ M $^{-1}$ S $^{-1}$)		k_{off} ($\times 10^{-1}$ S $^{-1}$)	
	- ATP	+ ATP	- ATP	+ ATP	- ATP	+ ATP
UvrB- β	2.6	0.4	2.0	1.5	5.2	0.6
TRCF- β	1.3	0.5	1.0	1.5	1.3	0.7